What is claimed is:

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the rpsL gene, selected from the group consisting of a

a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,

c) polynucleotide which is complementary to the polynucleotides of a) or b), and

d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

2. A polynucleotide as claimed in claim 1, wherein the polypeptide has the activity of the ribosomal protein S12.

3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a recombinant DNA which is capable of replication in coryneform bacteria.

4. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.

5. A polynucleotide as claimed in claim 3, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

6. A DNA as claimed in claim 3, which is capable of replication, comprising

(i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii), and, optionally,

(iv) sense mutations of neutral function in (i).

7. A DNA as claimed in claim 6, which is capable of replication, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.

8. A polynucleotide sequence as claimed in claim 1, which codes for a polypeptide which comprises the amino acid sequence shown in SEQ ID No. 2.

9. A coryneform bacterium in which the rpsL gene is enhanced.

10. The coryneform bacterium of claim 9, wherein the rpsL gene is over-expressed.

11. The Corynebacterium glutamicum strain DM1545 deposited as DSM 13992 at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (DSMZ, German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany).

12. A process for the fermentative preparation of an L-amino acid, comprising:

a) fermenting coryneform bacteria which produce the L-amino acid and in which at least the rpsL gene or nucleotide sequences which code for it are enhanced,

b) concentrating the L-amino acid in the medium or in the cells of the bacteria, and

c) isolating the L-amino acid.

13. A process as claimed in claim 12, in which at least the rpsL gene or nucleotide sequences which code for it are over-expressed.

14. A process as claimed in claim 12, wherein the L-amino acid is L-lysine.

15. A process as claimed in claim 12, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

16. A process as claimed in claim 12, wherein bacteria in which the metabolic pathways which reduce the formation of the L-amino acid are at least partly eliminated are employed.

17. A process as claimed in claim 12, wherein the bacteria are transformed with a plasmid vector, wherein the plasmid vector carries the nucleotide sequence which codes for the rpsL gene.

18. A process as claimed in claim 12, wherein the expression of the polynucleotide(s) which code(s) for the rpsL gene is enhanced.

19. A process as claimed in claim 12, wherein the expression of the polynucleotide(s) which code(s) for the rpsL gene is over-expressed.

20. A process as claimed in claim 12, wherein the regulatory/catalytic properties of the polypeptide for which the polynucleotide rpsL codes are increased.

21. A process as claimed in claim 12, wherein in the bacteria one or more of the genes selected from the group consisting of

the dapA gene which codes for dihydrodipicolinate synthase,
the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
the tpi gene which codes for triose phosphate isomerase,
the pgk gene which codes for 3-phosphoglycerate kinase,
the zwf gene which codes for glucose 6-phosphate dehydrogenase,
the pyc gene which codes for pyruvate carboxylase,
the mqo gene which codes for malate-quinone oxidoreductase,
the lysC gene which codes for a feed-back resistant aspartate kinase,
the lysE gene which codes for the lysine export protein,
the zwa1 gene which codes for the Zwa1 protein, and
the rpoB gene which codes for RNA polymerase B,

is or are enhanced or over-expressed.

22. A process as claimed in claim 12, wherein in the bacteria one or more of the genes selected from the group consisting of

the pck gene which codes for phosphoenol pyruvate carboxykinase,
the pgi gene which codes for glucose 6-phosphate isomerase,

the poxB gene which codes for pyruvate oxidase,

the zwa2 gene which codes for the Zwa2 protein

is or are attenuated.

23. A process as claimed in claim 12, wherein the bacteria are Corynebacterium glutamicum.

24. A coryneform bacterium which contains a vector which carries a polynucleotide as claimed in claim 1.

25. A process for discovering RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes which code for the ribosomal protein S12 or have a high similarity with the sequence of the rpsL gene, which comprises employing the polynucleotide comprising the polynucleotide sequences as claimed in claim 1 as a hybridization probe.

26. A process as claimed in claim 25, which is conducted on an array, micro array, or DNA chip.

27. A process for identifying a nucleic acid which codes for the ribosomal protein S12 or have a high similarity with the sequence of the rpsL gene, comprising:

contacting a sample with the polynucleotide sequence as claimed in claim 1 under hybridization conditions such that the polynucleotide sequence as claimed in claim 1 hybridizes with said nucleic acid when said nucleic acid is present in the sample.

28. The process of claim 27, wherein said nucleic acid is present in the sample.

29. The process of claim 28, further comprising isolating said nucleic acid.

30. The process of claim 27, wherein said nucleic acid is not present in the sample.

31. A DNA which originates from coryneform bacteria and codes for ribosomal S12 proteins, wherein the associated amino acid sequences between positions 38 to 48 in SEQ ID

No. 2 are modified by amino acid exchange.

32. A DNA which originates from coryneform bacteria and codes for ribosomal S12 proteins, wherein the associated amino acid sequences at position 43 in SEQ ID No. 2 contain any other proteinogenic amino acid excluding L-lysine.

33. A DNA which originates from coryneform bacteria and codes for ribosomal S12 proteins, wherein the associated amino acid sequences at position 43 in SEQ ID No. 2 contain L-histidine or L-arginine.

34. A DNA as claimed in claim 31, which codes for the ribosomal protein S12, the amino acid sequence of which contains L-arginine at position 43, shown in SEQ ID No. 4.

35. A DNA as claimed in claim 31, which contains the nucleobase guanine at position 128 of the coding region, corresponding to position 627 of the sequence shown in SEQ ID No. 3.

36. A coryneform bacterium which contains a DNA as claimed in claim 31.

37. A coryneform bacterium which contains a DNA as claimed in claim 32.

38. A coryneform bacterium which contains a DNA as claimed in claim 33.

39. A coryneform bacterium which contains a DNA as claimed in claim 34.

40. A coryneform bacterium which contains a DNA as claimed in claim 35.